

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 4, 1999, 03:34:45 ; Search time 1417.33 Seconds

(without alignments)
4586.373 Million cell updates/sec

Title: US-09-034-286-64

Perfect score: 1817

Sequence: 1 ACAGAGACACAGCGCTGTC.....GGAAAAAAAAAAAAAAAAAAAA 1817

Scoring table: IDENTITY_NUC

Searched: 808301 segs, 1788773984 residues

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43: gb_pr3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

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2	1772	97.5	2887	36	AF035528	AF035528 Homo sapi
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4	1491	82.1	1491	12	AF037469	AF037469 Homo sapi
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8	832.4	45.8	1280	12	HSU59914	HSU59914 Human chrom
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21	282.8	15.6	1431	5	XLJA3136	AJ003136 Xenopus l
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ALIGNMENTS

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DEFINITION AF035528
ACCESSION g2736315
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 2887)
Hata,A., Iagna,G., Massague,J. and Hemmati-Brivanlou,A.
the Smad4 tumor suppressor
Smad6 inhibits Bmp/Smad1 signaling by specifically competing with
Genes Dev. (1997) In press
2 (bases 1 to 2887)
Hata,A., Iagna,G., Massague,J. and Hemmati-Brivanlou,A.
Direct Submission
Submitted (21-NOV-1997) Laboratory of Molecular Embryology, The
Rockefeller University, 1230 York Avenue, New York, NY 10021, USA
JOURNAL
TITLE
AUTHORS
REFERENCE
FEATURES
Source 1. 2887

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RESULT 2
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DEFINITION AF035528
ACCESSION 92736315
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1 (bases 1 to 2887)
Hata,A., Laguna,G., Massague,J. and Hemmati-Briuanlou,A.
Smad6 inhibits BMP/Smad1 signaling by specifically competing with
the Smad4 tumor suppressor
Genes Dev. (1997) In press
2 (bases 1 to 2887)
Hata,A., Laguna,G., Massague,J. and Hemmati-Briuanlou,A.
Direct Submision
Submitted (21-NOV-1997) Laboratory of Molecular Embryology, The
Rockefeller University, 1230 York Avenue, New York, NY 10021, USA
JOURNAL
TITLE
AUTHORS
JOURNAL
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RESULT 3
AF043640
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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

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Homo sapiens Smad6 (SMAD6) mRNA, complete cds.
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92828711
human.
Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Carnivorini; Homnidae; Homo.
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Moren, A.
Direct Submission
Submitted (20-JUN-1998) Ludwig Institute for Cancer Research, Bow
595, Uppsala 751 24, Sweden
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AF037469 1491 bp mRNA PRI 02-DEC-1998
LOCUS Homo sapiens Smad6 (Smad6) mRNA, complete cds.
DEFINITION AF037469
ACCESSION 93941317
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1491)
Hagiwara, K., Freeman, A. H., McMenamin, M. G., Bennett, W. P.,
Nakashima, M., Minter, A. R., Yang, K., Takenoshita, S. and Harris, C. C.
Direct Submission
Submitted (09-DEC-1997) LHC, NIC, Building 37, Room 2C22 37 Convent
Drive, Bethesda, MD 20892, USA
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JOURNAL
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Query Match 82.1%; Score 1491; DB 12; Length 1491;
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AF037469 1491 bp mRNA PRI 02-DEC-1998
 LOCUS Homo sapiens Smad6 (Smad6) mRNA, complete cds.
 DEFINITION AF037469
 ACCESSION 93941317
 NID
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1491)

REFERENCE
 AUTHORS Nagaiwara,K., Freeman,A.H., McMenamin,M.G., Bennett,W.P.,
 Nagaiwara,M., Munter,A.R., Yang,K., Takenoshita,S. and Harris,C.C.
 Direct Submission

TITLE Submitted (09-DEC-1997) IHC, NIC, Building 37, Room 2C22 37 Convent
 Drive, Bethesda, MD 20892, USA
 JOURNAL

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RESULT 7
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 ACCESSION AF010133
 VERSION 92507639
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 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1488)
 AUTHORS Imanura,T., Takase,M., Nishihara,A., Oeda,E., Hanai,J.-I.,
 Kawabata,M. and Miyazono,K.
 TITLE Smad6 inhibits signalling by the TGF-beta superfamily
 JOURNAL Nature 389 (6651), 622-626 (1997)
 MEDLINE 97474481
 REFERENCE 2 (bases 1 to 1488)
 AUTHORS Takase,M., Kawabata,M. and Miyazono,K.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUN-1997) Biochemistry, The Cancer Institute of
 Tokyo, 1-37-1 Kami-Ikebukuro, Toshima-ku, Tokyo 170, Japan
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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 387 GGGGAGCTGCGCTGGAGGCTGCGTAATGTACCCGCCATGGACC-----434
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QY 807 AGCCGCGCGCGAGCTGTGCTGCGCGCGCTCTTTCGAGGCCGAGACTGACAGCAG 866
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Db 434 -----CTCTCTACTCTCTCTGTGTGAGACTTTCGCGTGGCGCGAGCTGACAGTAC 485
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 867 CCGTGAGACTGAAGCCCTGTGCGGCTGCGACAGCTTGCCG--CGCGCGCGAGCGCC 923
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QY 1044 CATGTCTTACACTGAAGAGAGGCTACCACTCCCTCATCTACTGTCTCGGCTGAATTCT 1103
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QY 1164 GGGAGCACCAGCGCGCTGTGGCGCGCTCTATGCGGTGTAGCAGAGCGCTCAGCATCT 1223
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QY 1284 GCGAGTGTGCGGCGCAAGCGCGAGCAAGATGCGCTTGGCATCCCTGACGACAGAGC 1343
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Db 897 GCGAGGCGGAGCGAGCAAGAGGAGGAGATTTGACTTGGATATGATTGAGCGGAGAGA 956
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QY 1404 TGGAGCGCGCGCGCGCGCGCGCTGTGCTGCGCAAGGTGCCCCCGGCTACTCATCA 1463
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RESULT 11
AF035529      848 bp      mRNA      VRT      01-JAN-1998
LOCUS      Xenopus laevis Smad6 mRNA, partial cds.
DEFINITION      AF035529
ACCESSION      92736317
NID
KEYWORDS
SOURCE
ORGANISM
    African clawed frog.
    Eukaryotes; Metazoa; Chordata; Vertebrata; Amphibia; Batrachia;
    Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus.
REFERENCE
    Hata,A., Laguna,G., Massague,J. and Hemmati-Briavanlou,A.
    Smad6 inhibits BMP/Smad1 signaling by specifically competing with
    the Smad4 tumor suppressor
    Genes Dev. (1997) in press
JOURNAL
    2 (bases 1 to 848)
AUTHORS
    Hata,A., Laguna,G., Massague,J. and Hemmati-Briavanlou,A.
TITLE
    Direct Submission
SUBMITTER
    Submitted (21-NOV-1997) Laboratory of Molecular Embryology, The
    Rockefeller University, 1230 York Avenue, New York, NY 10021, USA
FEATURES
    Location/Qualifiers
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            BAARIRKIGLIVLSRETDGVAWVNRSDHPIFVNSPFLDAPACRPLVYRKWPGY
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BASE COUNT      195 a      255 c      218 g      180 t

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Db	1877	GCAGCCGCCCTCGTCTCTACTCGGTCCGCCCTCTCGTGTGACAAAGTTCAGGTGGCCGA	1936
QY	856	CGTGCAGACGCGCGTGGAGCTGAAGCCCTGTGCGGCTGCCACAGCTTGCCGCCGCCGC	915
Db	1937	TCTCAGGCAATCTCTCGGAAGTCAAGAGCGCTGTGTGCTGTGAACTTACGGGAAGATCAA	1996
QY	916	CGACGGCCCTACCGTGTGTCTGCAACCCCTTACACTTCACCGGGGCTGTGGGGCCGATC	975
Db	1997	CCCCGAC--TGGTGTGTGTGCMAACCCCATCACTTATCTGACTGTGGAATAGAGTCT	2053
QY	976	TCCGCCACCTCCCTACTCTCGGCTGTCTCTCGCAGAGTATCAAGCACTGATCTGTC	1035
Db	2054	TCCCCCTCTCTCTTACTTACCAGATACCCATGGATTTTTCACAAACAACTGCAGGCTGCC	2113
QY	1036	CGATTCCACATTGTCTTACACTGAAGGAGGCTACCACTCCCTCATCATCTGCTCGGG	1095
Db	2114	AGATGTGTACTCTCTCCGCCGGAACCGGGGAAGAAATATATCT-----GGCCCCG	2167
QY	1096	TGAATTCAGACGCCAGCATGTCTCCGAGCGCACCAAGCCGAGCCACTGGTGTGAGGT	1155
Db	2168	GGGGCTTTCAGATATCCCAATCTTCTTGTGAAGCTGTGGATTCGCTGACACTGGTGTGGT	2227
QY	1156	GGGCTACTGGAGACACGGAGCGCGCTGGGGCCGCTCTATGGGGTGTAGACAGGCGCT	1215
Db	2228	GGCATCTGGGAGAGAAAGACTGCGCTGGGAGAGCTCTACTGTGTCCAAAGCCCTCCT	2287
QY	1216	CAGCATCTTCTACGACCTTACTCTCAGGGGACAGCGGCTTCTGCTGTGGCCAGCTCAACCTGA	1275
Db	2288	GGATATCTTCTATGATCTACTCTAGGGGAATGCTTTGCTGTGGACACTCAATTCGGA	2347
QY	1276	GCAAGCCAGCGAGTGGTGGCGGCAACCGCGCAAGATTCGGCTTGGCATCTCTCTAG	1335
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QY	1336	CAGAGACCCGAGGGGTGTGGGCTTACAAACGGCGGCGAGCAACCCATTTGTGACATC	1395
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QY	1396	CCCGACCTGGACGCGCGCGCGCGCGCGCTGTGTGTGCGCAAGTGCCTCCCGGCTA	1455
Db	2468	CGCCACACTGGACAAACCCGGAATCTCAAGAGCGTGTGTGGTGCACAAAGTGTCTCCGTGT	2527
QY	1456	CTCCATCAAGGTGTGTGACTTGCAG--CGCTGGGCTGTGACAGCAGCGCCCGAGCGGA	1513
Db	2528	CTCCATCAAGGCTTTTGTACTATGAAAGGCTTACAGCTGTGACAGCGCCCAATGACCACTGA	2587
QY	1513	CGCCGCGAGGGCCCTTACGACCCCAACAGAGTTCGGCATATGTTTGGCAAGGCTGGGG	1572
Db	2588	GTTCATGCACAAACCAATGAGAGGGGTTTACCGGTGACAGATACGTTTGTAAAGGGCTGGGG	2647
QY	1573	GCCCTGTACATCCCGGAGTTTCAATCACTTCCTCCCTGTGGCTGGAGATCTCTCTCA	1637
Db	2648	CCAATGCTTACACCCGCAATTCATCAGCAGCTCCCGTGTGTGGAGTGTATCTTCA	2707
QY	1633	CAACC 1637	
Db	2708	CAGCC 2712	
RESULT	13		
LOCUS	AF015260	1281 bp	RNA
DEFINITION	Mus musculus	Smad7 mRNA, complete cds.	ROD
ACCESSION	AF015260		21-OCT-1997
KEYWORDS	92460039		
ORGANISM	house mouse.		
REFERENCE	Eukaryote: Metazoa: Chordata: Vertebrata: Mammalia: Eutheria:		
AUTHORS	Rodentia: Sciurognathi: Muridae: Murinae: Mus.		
	1 (bases 1 to 1281)		
	Nakao, A., Aitakhte, M., Moren, A., Nakayama, T., Christian, J.L.,		

FEATURES	source
TITLE	Heuchel, P., Itoh, S., Kawabata, M., Heldin, N.E., Heldin, C.H. and ten Dijke, P.
JOURNAL	Identification of Smad7, a TGFbeta-inducible antagonist of TGF-beta signalling
MEDLINE	Nature 389 (6651), 631-635 (1997)
REFERENCE	2 (bases 1 to 1281)
AUTHORS	Nakao, A., Morian, A., Heuchel, R., Itoh, S., Heldin, C.-H. and ten Dijke, P.
TITLE	Direct Submission
JOURNAL	Submitted (21-JUL-1997) Ludwig Institute for Cancer Research, Uppsala Branch, Box 593, Biomedical Center, Uppsala 75124, Sweden
source	Location/Qualifiers
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	1. .1281
	/note="TGF beta-induced signal response inhibitor"
	/codon_start=1
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	/db_xref="PID:g2460040"
	/translation="MFRTRKSLVRLMRSPAGCEDEEEGGGGGGLRGEGATP GRATGAGGGGGRAGCCLGKARGAKGHHNHPPTSGAGAGAGADKLATHSVLLK LKEQLDLLLAQVSRGSTRACLLDGRICDRCRPARAQAOPAPRSSSLDLL LKFWPDPDRHSSEYKRLCCCSYKRIKPELDCRPHHSRCELESPPPSYSRIPMD LKPPAGCPDAVPSSAETGGTNYLAPGGLSDSQLLEPEDRSHMCVVAWEKTRGR YCSVEPSIDIFYDLDPONGFCLGQINDSKSLQAVKASKIGCIGQLREVDGWWYN RSSEPIFKSATLNDPSRSLVLHKKVEPFSEIKAFDEKAYSLORPNDEHMOOPWIG FTVVISFVKGGCCYTRQFISSCCMVEIENSR"

Query Match	16.0%	Score 290.2	DB 13	Length 1281
Best Local Similarity	54.8%	Pred. No. 3.8e-30		
Matches 693; Conservative	0	Mismatches 548	Indels 24	Gaps 5

Oy 382 CGCCAGGGGCGGGAGAGCGCCGCGAGCGGGGGCGCCCCCGAGGCCCTATGTCGAGGCC 44.1
 Db 27 GTCGCGGGGTCTCTGGAGAGACCGCTGCGCCCGCGCGAGAGACGAGAGAGGCGTGGG 85
 Oy 442 AGGGGCGCGGCTGGAGAGCTCCCTGCTGAGAGTGGCGAGCCGGAGAGCCCGGGCTGGCT 50.1
 Db 87 GGGTGGCGCGGAGAGAGCGCAGCTGCGGGGAGAAAGGGGGCCAGCAGCGCCGGGCTTATGG 146
 Oy 502 GCCCAGAGTACTGCGAGAGCGGTGAGACTGCTGTCCTCTTTTCGAGCGGGAGCGCCGCGG 56.1
 Db 147 GSGCTGTGGGCGGGGTGGGGCAGAGGGGTGGTGTGCTGGCGCAAGCAGATCCGAGGTGC 206
 Oy 562 CGCGCCCCGGGAGCGCCAGCCAGCCCCCTGAGCCGGGGCGGCGCTGAGAGCCGCGGGCGG 62.1
 Db 207 CAAGAGTCACCAACCATCCCATCCCCAACTCGGGTGGCGGGCGGCGCCGGGGGCGCGGA 266
 Oy 622 GCGAGTGGCGAAGGGGCGCTGCGGGGCTGCTGCTCTGAGAGGAGAACTCAAAACCGTCAC 68.1
 Db 267 GCGGATGTGAAGGGGCTCACGCACTCGGTCTCA-----AGAAACTCAAGAGACGCGCA 320
 Oy 682 GTACTCGCTGTGTAAGCGCGCTCAAGAGACGCTGCTGAGACCGTGTGAGAGCGGTGGA 74.1
 Db 321 GCTGGAGCTGCTGCTTACAGCGCGGTGGAGATCCCCGGGGGTATACGGCAGCCGCTGCTCT 380
 Oy 742 GTGCCCGCGCGAGCGTGGCGGGCGGCGTGGCTGATGATCGCGCGCGCAGCACTCCGCTGGG 80.1
 Db 381 GTGTGCGCGCGCGCTGAGACTCAGAGGTGGGCGCGGGGGGCGGCCAGCGGGCAGCCCGC 444
 Oy 802 CGGCGACGCGG-----CGCGCGCACTGCTGCTGCGCGCGCTCTTTGCTGCTGGCCGA 85.5
 Db 441 GCAGCGCGCTCTGCTCTACTGCTCTCCCTCTGCTGCTGCTGCAAACTGTTCAAGTGGCCGA 500
 Oy 856 CCTGAGAGACGCGGTGAGAGCTGAAGCCGCTGGGCGCGCACAGCTTCGCGCGCGCGCG 91.5
 Db 501 TCTCAGGATTCCTCTGGAGTCAAGAGGCTGTGTTGCTGTGAATCTTACGGGAAGATCAA 560

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Db 864 ---TGTGTCTGTGCAACCCCATCACCTTACCCACTCTGTGGAAGTCTGAGTCTCCCCCC 920
QY 984 CTCCTACTCTGTGGCTGTCTCTCTGCGAGAGTACAAAGCCATGATCTCCGATTCCA 1043
Db 921 CTCCTACTCTGAGTACCCCATGATGATTTCTCAACCAACTGCAAGTCTCCAGATCTG 980
QY 1044 CATTTCTTACACTGAAGAGGAGTACCAACTCCCTCATCTGCTCCGGTGAATTC 1103
Db 981 TGCCCTTCTCCGCTGAACAGGGGAACGATATCT-----GGCCCTGGGGGCTTT 1034
QY 1104 CAGAGCCGCAATGTCTCCGAGCCCAAGCCAGCCAGCTGTGTCAGCTGTGCTACT 1163
Db 1035 CAGATTTCCCACTTCTTGTGAGCTTGGGGATCGGTACACTGTGTGCTGTGCTACT 1094
QY 1164 GGGAGCACCAGAGCGCGGGGCTCTATGCGGTGTACAGCCAGGCGCTCAGCATCT 1223
Db 1095 GGGAGAGAAAGACGAGAGTGGGAGCTTACTGTCTCAGAGCCCTCTGTGATATCT 1154
QY 1224 TCTACGACTTACTCAGGAGCAGCGCTTGTGCTGGGCCAGCTCAACCTGGAGCAGCGCA 1283
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QY 1284 GCGAGTGGGTGGCGGCAACCGCAAGATCGGCTTGGGATCTGTCTCAGCAAGAGC 1343
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Search completed: May 4, 1999, 03:35:35
Job time: 2243 sec

Tue May 4 11:46:44 1999

US-09-034-286-65.rspt

Page 2

IMMATURE ET AL

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RESULT 2
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DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE SMAD6
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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RA HARA A., LAGUNA G., MASSAGUE J., HEMMATI-BRIVANTLOU A.;
RL GENES DEV. 0:0-0(1997).
DR EMBL: AF035528; G2736316;
SQ SEQUENCE 496 AA; 53496 MM; B0709066 CRC32;
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Query Match 99.9%; Score 3627; DB 4; Length 496;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 495; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MFRSKRGGLVRLMRSRVPPVREGSGGGGDEDSLSGRAPAPARAREGGCGSSEV 60
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QY 121 KRLKERSLDITLLEAVESRGVPGCVLPBRADRLGGOAPAPOLLGLRFRMPDLOHAE 240
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RESULT 3
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AC 035182:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE MAD HOMOLOG 7 (SMAD6).
GN MAD7 OR MSAD6.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE: 97474481.
RA IMAMURA T., TAKASE M., NISHIHARA A., OEDA E., HANAI J.-I., KANABATA M.,
RT "Smad6 inhibits signalling by the TGF-beta superfamily."
RL NATURE 389:622-626(1997).
DR EMBL: AF010133; G2507640;
DR MGD: MGI:1100516; MADH7.
DR PPM: PF00968; Dwaflin; 1.
SQ SEQUENCE 495 AA; 53714 MM; 0C0B42D1 CRC32;
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Query Match 92.3%; Score 3349; DB 11; Length 495;
Best Local Similarity 93.0%; Pred. No. 0.00e+00;
Matches 463; Conservative 14; Mismatches 16; Indels 5; Gaps 4;

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QY 121 KRLKERSLDITLLEAVESRGVPGCVLPBRADRLGGOAPAPOLLGLRFRMPDLOHAE 239
DB 179 LKRLKERSLDITLLEAVESRGVPGCVLPBRADRLGGOAPAPOLLGLRFRMPDLOHAE 238
QY 179 LKRLKERSLDITLLEAVESRGVPGCVLPBRADRLGGOAPAPOLLGLRFRMPDLOHAE 238
DB 240 VELKPLCGCHSFPAADGPTVCCNPFHFSRLCGPESPPEPYSLSPBDYKPLDLSDSL 299
QY 240 VELKPLCGCHSFPAADGPTVCCNPFHFSRLCGPESPPEPYSLSPBDYKPLDLSDSL 299
DB 239 VELKPLCGCHSFPAADGPTVCCNPFHFSRLCGPESPPEPYSLSPBDYKPLDLSDSL 298
QY 239 VELKPLCGCHSFPAADGPTVCCNPFHFSRLCGPESPPEPYSLSPBDYKPLDLSDSL 298
DB 300 SYTETATNSLITAPGEFSDASMPDAPKPSHWCVAWEHRTVRGLYAVDAQVSTFY 359
QY 300 SYTETATNSLITAPGEFSDASMPDAPKPSHWCVAWEHRTVRGLYAVDAQVSTFY 359
DB 299 SYTETATNSLITAPGEFSDASMPDAPKPSHWCVAWEHRTVRGLYAVDAQVSTFY 358
QY 299 SYTETATNSLITAPGEFSDASMPDAPKPSHWCVAWEHRTVRGLYAVDAQVSTFY 358
DB 360 DEPOSGFCLOLNEQRESESVRTRRSKIGFILLSKPEPDVWYVWYVNGEHPITFVNSPTLD 419
QY 360 DEPOSGFCLOLNEQRESESVRTRRSKIGFILLSKPEPDVWYVWYVNGEHPITFVNSPTLD 419
DB 359 DEPOSGFCLOLNEQRESESVRTRRSKIGFILLSKPEPDVWYVWYVNGEHPITFVNSPTLD 418
QY 359 DEPOSGFCLOLNEQRESESVRTRRSKIGFILLSKPEPDVWYVWYVNGEHPITFVNSPTLD 418
DB 420 AAGGALVVRKVPYSGYSIKVFEDERSGLOHAPEDPAADGPPYVNSVRSISFAKMGPCYSR 477
QY 420 AAGGALVVRKVPYSGYSIKVFEDERSGLOHAPEDPAADGPPYVNSVRSISFAKMGPCYSR 477
DB 419 AAGGALVVRKVPYSGYSIKVFEDERSGLOHAPEDPAADGPPYVNSVRSISFAKMGPCYSR 478
QY 419 AAGGALVVRKVPYSGYSIKVFEDERSGLOHAPEDPAADGPPYVNSVRSISFAKMGPCYSR 478
DB 478 OPTSCPCWLEILLNPR 495
QY 478 OPTSCPCWLEILLNPR 495
```

RESULT 4
ID 015799: PRELIMINARY: PRT: 235 AA.
AC 015799:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SMAD6.
OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96259564.
RA RIGGINS G.J., THIAAGALINGAM S., ROZENBLUM E., WEINSTEIN C.L., KERN S.E.,
RA HAMILTON S.R., WILSON J.R., MARKOWITZ S.D., KINZLER K.W.,
RA VOGELSTEIN B.;
RT "Mad-related genes in the human.";
RL NAT. GENET. 13:347-349(1996).
DR EMBL; U59914; G1654327; -
DR PIRAM; PF00968; Dwarfin; 1.
SQ SEQUENCE 235 AA; 26235 MW; F696E2F2 CRC32;
Query Match 45.3%; Score 1646; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 4, 84e-303; Mismatches 0; Gaps 0;
Matches 223; Conservative 0; Indels 0; Gaps 0;
Db 13 SPPEYSLRSPDEKPLDLSSTLSTETATNSLTAPGEFSDASMPDAPKPSHWS 72
OY |||||||
OY 274 SPPEYSLRSPDEKPLDLSSTLSTETATNSLTAPGEFSDASMPDAPKPSHWS 333
OY |||||||
OY 73 VAYVHRTVGRRLAVYQAVSIFDLPQSGGFCGLQNLKORSVARTSKIGFILL 132
OY |||||||
OY 334 VAYVHRTVGRRLAVYQAVSIFDLPQSGGFCGLQNLKORSVARTSKIGFILL 393
OY |||||||
Db 133 SKEPDGVAAYNGEHPITVNSPTLDAPGGRALVYKVPYSGYIKVFDEERSGLOHAPPD 192
OY |||||||
OY 394 SKEPDGVAAYNGEHPITVNSPTLDAPGGRALVYKVPYSGYIKVFDEERSGLOHAPPD 453
OY |||||||
Db 193 AADPYDPSVYRISFAKMGPCYSROFTSCPCWLEILLNPR 235
OY |||||||
OY 454 AADPYDPSVYRISFAKMGPCYSROFTSCPCWLEILLNPR 496
OY |||||||
RESULT 5 PRELIMINARY; PRT; 280 AA.
ID 057475;
AC 057475;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE SMAD6 (FRAGMENT).
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-HEAD;
RA HATA A., LAGNA G., MASSAGUE J., HEMMATI-BRIVANDOU A.;
RL GENES DEV. 0:0-0(1997).
DR EMBL; AF035529; G2736318; -
FT NON_TER 1
SQ SEQUENCE 280 AA; 31094 MW; 685518EF CRC32;
Query Match 41.5%; Score 1508; DB 13; Length 280;
Best Local Similarity 70.5%; Pred. No. 2, 00e-274; Mismatches 31; Indels 6; Gaps 4;
Matches 196; Conservative 45; Mismatches 31; Indels 6; Gaps 4;
Db 4 HGPFFLLLCRLFRWPELOHPQOLKALSGCAGGSSNNCCCNPHYHSCVCEPSP 63
OY :|||||
OY 218 QPAPQLLGLRFRWPDLOHVELKPLCGCHSFAAADGPTVC-NPHYHSLCGPESBP 276
OY |||||||
Db 64 PPSYLSKIKQKPLDLSDS--YTEMASNSLCTIADISTSLSPMSKQGHWCVA 120
OY |||||||
OY 277 PPSYLSKIKQKPLDLSDS--YTEMASNSLCTIADISTSLSPMSKQGHWCVA 336
OY |||||||
Db 121 WEHRRVRLVAVCPSYIFDLPQSGGFCGLQNLKORSVARTSKIGFILL 180
OY |||||||
OY 337 WEHRRVRLVAVCPSYIFDLPQSGGFCGLQNLKORSVARTSKIGFILL 396
OY |||||||
Db 181 TDGVAAVNRSDHPITVNSPTLDAPACRPLVYKVPYSGYIKVFDEERSGLOHAPPD 240
OY |||||||
OY 397 PDGVAAVNRSDHPITVNSPTLDAPACRPLVYKVPYSGYIKVFDEERSGLOHAPPD 454
OY |||||||

Db 241 TDGPYDPSVYRISFAKMGPCYSROFTSCPCWLEILL 278
OY :|||||
OY 455 ADGPYDPSVYRISFAKMGPCYSROFTSCPCWLEILL 492
OY |||||||
RESULT 6 PRELIMINARY; PRT; 382 AA.
ID 057459;
AC 057459;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SMAD7.
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98119796.
RA NAKAYAMA T., SNYDER M.A., GREWAL S.S., TSUNEIZUMI K., TABATA T.,
RA CHRISTIAN J.L.;
RT "Xenopus Smad8 acts downstream of BMP-4 to modulate its activity
RT during vertebrate embryonic patterning.";
RL DEVELOPMENT 125:857-867(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA BHUSHAN A., CHEN Y., VALE W.;
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF026125; G3158344; -
DR EMBL; AF045742; G3005093; -
SQ SEQUENCE 382 AA; 42713 MW; 22E7791D CRC32;
Query Match 36.2%; Score 1315; DB 13; Length 382;
Best Local Similarity 53.0%; Pred. No. 1, 51e-234; Mismatches 174; Conservative 71; Mismatches 75; Indels 8; Gaps 6;
Matches 174; Conservative 71; Mismatches 75; Indels 8; Gaps 6;
Db 58 ELKALHCVLKKLEKOKLEGLOAVCKGARGSCILLPAKLDLSRGOAFSLPLLLCK 117
OY |||||||
OY 171 ELKTVTLRLKRLKRLSDTLLEAVESRGVPGGCVLVRDL--RLGQAPQOLLGR 228
OY |||||||
Db 118 VFRPDLRHSVDVRLSCDSYGRN-NPELLCCPNHLISRLCELESPPYTRY-PMDFL 175
OY :|||||
OY 229 LFRPDLRHSVDVRLSCDSYGRN-NPELLCCPNHLISRLCELESPPYTRY-PMDFL 288
OY |||||||
Db 176 KPLADSPSVSSSTETGTNL--APEGLDSQLLHETGDSHNCMAVWEKTRVGR 233
OY |||||||
OY 289 KPLADSPSVSSSTETGTNL--APEGLDSQLLHETGDSHNCMAVWEKTRVGR 347
OY |||||||
Db 234 SVQEPSLIDFYDLPQSGGFCGLQNLKORSVARTSKIGFILLKREVDGVVYVNRSS 293
OY :|||||
OY 348 SVQEPSLIDFYDLPQSGGFCGLQNLKORSVARTSKIGFILLKREVDGVVYVNRSS 407
OY |||||||
Db 294 YPIFKSATLDPDPSRLTLVHKEVPGESIKAFDEKAYSLORPDHDEMQPMTGTVQI 353
OY |||||||
OY 408 YPIFKSATLDPDPSRLTLVHKEVPGESIKAFDEKAYSLORPDHDEMQPMTGTVQI 466
OY |||||||
Db 354 SFVAGWGOCYTRQFISSCPCWLEVIYFN 381
OY |||||||
OY 467 SFVAGWGOCYTRQFISSCPCWLEVIYFN 494
OY |||||||
RESULT 7 PRELIMINARY; PRT; 382 AA.
ID 057522;
AC 057522;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE SMAD7.
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
RN [1]

RP SEQUENCE FROM N.A.
RA CASELLAS R., HEMMATI-BRIVANTOU A.:
RL SUBMITTED (JAN-1998) TO EMBL/GENEBANK/DBJ DATA BANKS
DR EMBL: AF042198; G2921581; -
SQ SEQUENCE 382 AA: 42729 MW; 655E5184 CRC32;

Query Match	35.68;	Score 1293;	DB 13;	Length 382;
Best Local Similarity	52.48;	Pred. No. 5.16e-230;		
Matches 172;	Conservative	70;	Mismatches 78;	Indels 6

[illegible]

ID	RESULT	PRELIMINARY:	PRT:	425 AA.
AC	088709			
AD	088709			
DT	01-NOV-1998	(TREMBLEL. 08, CREATED)		
DT	01-NOV-1998	(TREMBLEL. 08, LAST SEQUENCE UPDATE)		
DT	01-NOV-1998	(TREMBLEL. 08, LAST ANNOTATION UPDATE)		
DE	MAD-RELATED	PROTEIN SMAD7B.		
GN	SMAD7B.			
OS	MUS MUSCULUS (MOUSE).			
OC	EURYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;			
NC	ROENTIIA; SCIROGNAHI; MURIDAE; MURINAE; MUS.			
NC	[1]			
NC	SEQUENCE FROM N.A.			
PC	TISSUE-WHOLE EMBRYOS;			
RA	KITAMURA K., OKAZAKI K.;			
RT	"Isolation of cDNAs encoding mouse homologues of Mad (Smad7 and			
RT	Smad7) that can mediate TGF-beta family signalling."			
RL	SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL; AJ000551; E1313655; .			
FT	VARIANT	232	V -> A (IN REF. 1).	
SO	SEQUENCE	425 AA;	46598 MW;	4EECD29 CRC32;

	Query Match	34.3%	Score 1245;	DB 11;	Length 425;
	Best Local Similarity	53.8%	Pred. No. 3,926-220;		
	Matches 183;	Conservative	65;	Mismatches 74;	Indels 18; Gaps 9
Db	89	EADKALHSHVLKRIKEQLELLIQAVESRGRTACLLPGRUDCRIGPAPASAPQAQ	148		
	169	EQELKTVYSLIKRKERSLDTLLEAVESRGVGGCVLP-RADLRIG-G-----QPA	220		
Db	149	PPSSVLELLCKFRPMDLHSHSEVKRLCCESYGR-I-NPELYCCNPHILSRICELESP	207		
QY	221	PP-----QLLGRLEFRPMDIQHAEVKPLRCGCHSFAAAGSPYCCNPHFSRLCGESP	275		
Db	208	PPPYSR-I-PMDFLKPTGCPDAVPSSVVTGGTNYL--APGGISDQQLLEPGRDSHMCVVA	264		
QY	276	PPPYSRISPPREDEYKPLDLSDSITLSYETEAMNSLITRNAGEFSDSAMSPDITAKSHMCVVA	335		

Db .265 YWEETPRGRILYQWQESBLDFYDLPGQNGCCLQOLNSDNKSQLVORVRSKIGGCIOLTR 324
 |||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 325
 QY 336 YWEHTPRGRILYAYDDAVSIFYDLPGSGCGLQOLNLEQSESVRRTRRSIGGICLLSK 395
 |||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 396
 Db 325 EVDGWWVYVNRSSYPILFKSATLMDPDSRTLLYHNVFEGESTKAFDYKAVSLORPNDHEF 384
 | ||| |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: 385
 QY 396 EPDGYMAVNRSEHPILFNVSPTLLAPGGRAALVVRKVPYGIKVFDEFRS-GLQHAPEPDA 454
 ||| |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: 455
 Db 385 MOCPWTGFTVQVISFVKGAGCCTROFTSSCCMLEVIFNS 424
 : ||| |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: 425
 QY 455 ADGPYDPSVRSIPAKMGWCICISKQPTTSCPCMEIILLN 494

AC	015105;	PRELIMINARY;	PRT;	426 AA.
AD	015105			
DT	01-JAN-1998 (TREMBLREL, 05, CREATED)			
DT	01-JAN-1998 (TREMBLREL, 05, LAST SEQUENCE UPDATE)			
DT	01-NOV-1998 (TREMBLREL, 08, LAST SEQUENCE UPDATE)			
DE	MAD-RELATED GENE SMAD7.			
GN	SMAD7.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES			
OC	CATARRHINI; HOMINIDAE; HOMO.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	HAYASHI H., ABDOLLAH S., QUI Y., CAI J., XU Y.-Y., GRINNELL B.W.,			
RA	RICHARDSON M.A., TOPPER J.N., GIMBRONE M.A. JR., WRANA J.L., FALB D.;			
RL	CELL 0:0-0(1997).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 97404392.			
RA	TOPPER J.N., CAI J., QUI Y., ANDERSON K.R., XU Y.-Y., DEEDS J.D.,			
RA	FEELY R., GIENNO C.J., WOOLF E.A., TAYLOR O., MAYS G.G., SAMPSON B.A.,			
RA	SCHOEN F.J., GIMBRONE M.A. JR., FALB D.;			
RT	"Vascular MADS: two novel MAD-related genes selectively inducible by			
RT	flow in human vascular endothelium."			
RL	PROC. NATL. ACAD. SCI. U.S.A. 94:9314-9319(1997).			
DR	EMBL: AF010193; G2252832; -			
DR	PFAM: PF00968; Dwafrin:1.			
SO	SEQUENCE 426 AA; 46425 MW; 598F0022 CRC32;			

Query Match	34.2%;	Score 1242;	DB 4;	Length 426;
Best Local Similarity	54.0%;	Pred. No. 1.62e-219;		
Matches	184;	Conservative	66;	Mismatches 72;

[illegible]

RESULT	10		
ID	014740	PRELIMINARY;	PRT; 426 AA

DB 264 AYWEKTRVGRGLYCVQEPDIDFYDLPOGNGFCGLGOLNSDNKSLVQKNSKIGCGIOLT 323
 QY 335 AYWEHRTVGRGLYAVYQANISIFDLQGGSGFCGLGOLNLSRSESVRTRRSKIGFILLS 394
 DB 324 REVDGVAWVYRSTYPIFKATLNDNDPRLVHVKYPPGSEIKAFEDKXYSIORPDHE 363
 QY 395 KEPDGVAWVYRSTYPIFKATLNDNDPRLVHVKYPPGSEIKAFEDKXYSIORPDHE 363
 DB 384 FMOQPTGFTVYQSFVKGWGCCTROFISCPWLEVIENS 424
 QY 454 AADGPDVNSVSRISFAKMGWPCYSROFITSPCWLEILLNN 494

RESULT 13
 ID 015968 PRELIMINARY: PRT: 568 AA.
 AC 015968:
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE DAD POLYPEPTIDE.
 OS DROSOPHILA MELANOGASTER (FRUIT FLY).
 CC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
 CC PERMYCTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYROIDEA;
 CC DROSOPHILIDAE; DROSOPHILA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97474482.
 RA TSUNETSUMI K., NAKAYAMA T., KAMOSHIDA Y., KORBERG T.B.,
 RA CHRISTIAN J.L., TABATA T.,
 RT "Daughters against dpp modulates dpp organizing activity in Drosophila
 RT wing development."
 RL NATURE 389:627-631(1997).
 DR EMBL: AB004232; D1023711;
 DR PFAM: PF00968; Dwarfin; 1.
 SQ SEQUENCE 568 AA; 63605 MW; B414441E CRC32;

Query Match 14.2%; Score 515; DB 5; Length 568;
 Best Local Similarity 38.4%; Pred. No. 7.07e-73;
 Matches 113; Conservative 51; Mismatches 105; Indels 25; Gaps 18;

DB 281 PHYTASRLFWRELWNAKELKRLPTC--PAARDCIYMCNPLHMFRLHQEPESPTPP 337
 QY 222 PDLGLGLFWPDLQHLVHELKPLCGHSFAADGPRVCNPH-FSRLGPE--SEPP 278
 DB 338 YQSKMLRLKADAEEDSDQDAKSAISTASSTISNLYKALYESVTTDKDNHNS 397
 279 Y--SR-LSPRD-EYK--PL-DLSDSTLSTYETETATN-SLTAPGEFSDAKMSD-DATKPS 329
 DB 398 QVWCQIAYWEMARVGEFEFAKTNVAVITDGIYASEVSMCLADLTPAGNOIHVVPTA 457
 QY 330 H-WCSVAWYEHRTVGRGLYAVYQANISIFD--PQSGGFCGLGOLNLE-QRSESVRRT- 383
 DB 458 RTTVGIGVGLSLGNDGVWYINRGNTTIFVDSPTLSENDR--VC-KVPGYCYLKAETNR 514
 QY 384 REKIFGILLKEPDCGVMAVYNGEHPFVNSPTLDAPGRALVYKVPVPGYSIKVFDEFR 443
 DB 515 AELLNMRDGHHPGVYDFYSIKISFGKMGWGRDYKRODIMGPCWLEVHSLR 568
 QY 444 SGLQHAPEPDA-ADGPDVNSVSRISFAKMGWPCYSROFITSPCWLEILLNNPR 496

RESULT 14
 ID 091912 PRELIMINARY: PRT: 467 AA.
 AC 091912:
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE MAD2.
 GN MAD2.
 OS XENOPUS LAEYIS (AFRICAN CLAMMED FROG).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
 CC MESOBATRACHIA; PIPOIDEA; PIPOIDAE; XENODIDAE; XENODIDAE; XENODIDAE; XENODIDAE;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE: 96222291.
 RA GRAFF J.M., BANSAL A., MELTON D.A.;
 RT "Xenopus Mad proteins transduce distinct subsets of signals for the
 RT TGF beta superfamily."
 RL CELL 85:479-487(1996).
 DR EMBL: L77885; G1333645;
 DR PFAM: PF00968; Dwarfin; 1.
 SQ SEQUENCE 467 AA; 52411 MW; 1245ED6E CRC32;

Query Match 10.0%; Score 363; DB 13; Length 467;
 Best Local Similarity 32.3%; Pred. No. 7.73e-44;
 Matches 75; Conservative 57; Mismatches 88; Indels 12; Gaps 9;

DB 218 PETPPPGY--ISEDETSQDOLQSGMDIGSPALSPSTLS-PVN-HNLDQPVYTSSEAF 273
 QY 272 PESPPPPYRSLSPDEYKPLDLSSTLSTYETETATNLSITAPGEFSDAKMSDPA-TKPSH 330
 DB 274 WCSIAYVELNQRVGETHFASOPSILTVDFTPDSNSERFCLLSNVNATVEMTRRHIG 333
 QY 331 WCSIAYWYEHRTVGRGLYAVYQANISIFDLPQSGGFCGLGOLNLSRSESVRTRRSKIG 388
 DB 334 RGVRLYYIGEVFAECSDSAIFVQSPNCNRYGHPATYCKIPGCKLTFNNOEPAL 393
 QY 389 FGILLSKEPDGVMAVYNGEHPFVNSPTLDAPGR-ALVYKVPVPGYSIKVFDEFR-SGL 446
 DB 394 LAQSVNQGFEAVYQLTFRCTIRMSFVKGWGAERYRQTVTSNPGWIELHLNP 445
 QY 447 QHAPEPDAADPDV-PN-SVRSIFAKMGWPCYSROFITSPCWLEILLNNPR 495

RESULT 15
 ID 070436 PRELIMINARY: PRT: 467 AA.
 AC 070436:
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE SMAD2 PROTEIN.
 GN SMAD2.
 OS RATTUS NORVEGICUS (RAT).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 CC SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA OSAKI M., YONEKURA A., MIYAZAKI Y., HIROTA Y., ONO N., SONTA S.,
 RA NAKABA H., OHTSUKA A., TSUKAZAKI T., SHINDO H., YAMASHITA S.,
 RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
 RA ZHANG Y.-Q., KANZAKI M., KOJIMA I.;
 RT "Rat Smad2."
 RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF056001; G3025890;
 DR EMBL: AB017912; D1034419;
 SQ SEQUENCE 467 AA; 52239 MW; FD9EFE07 CRC32;

Query Match 9.9%; Score 361; DB 11; Length 467;
 Best Local Similarity 32.3%; Pred. No. 1.82e-43;
 Matches 75; Conservative 57; Mismatches 88; Indels 12; Gaps 9;

DB 218 PETPPPGY--ISEDETSQDOLQSGMDIGSPALSPSTLS-PVNHS-LDQPVYTSSEAF 273
 QY 272 PESPPPPYRSLSPDEYKPLDLSSTLSTYETETATNLSITAPGEFSDAKMSDPA-TKPSH 330
 DB 274 WCSIAYVELNQRVGETHFASOPSILTVDFTPDSNSERFCLLSNVNATVEMTRRHIG 333
 QY 331 WCSIAYWYEHRTVGRGLYAVYQANISIFDLPQSGGFCGLGOLNLSRSESVRTRRSKIG 388
 DB 334 RGVRLYYIGEVFAECSDSAIFVQSPNCNRYGHPATYCKIPGCKLTFNNOEPAL 393
 QY 389 FGILLSKEPDGVMAVYNGEHPFVNSPTLDAPGR-ALVYKVPVPGYSIKVFDEFR-SGL 446

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Page 7

D_b 394 LMSVNOGFEAVYQLTRMCTIRNSFVKGWGAERYRQTVTSPEWCIELHLNGP 445
 : ::::| | | | : | | | | : | |
Q_y 447 CHAPEPDADGPDP-PN-SVRISFAKGMGPCYSRQFITSCPCWLEILLNNP 495

Search completed: Fri Apr 30 20:39:41 1999
Job time : 104 secs.

